

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:58:35 ; Search time 60.5 Seconds
(without alignments)
1466.589 Million cell updates/sec

Title: US-10-757-863-4

Perfect score: 1169
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Published Applications_AA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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; Publication No. US2002004587A1
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; TITLE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREOF
; FILE REFERENCE: P1780R1
; CURRENT APPLICATION NUMBER: US/09/813,341
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/195,819
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-341-2

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; Sequence 2, Application US/10277370
; Publication No. US20030157108A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Glycoprotein Compositions
; FILE REFERENCE: P1877R1
; CURRENT APPLICATION NUMBER: US/10/277,370
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/337,642
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/347,694
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; ORGANISM: homo sapiens
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Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 22, 2005, 12:35:38 ; Search time 30 Seconds
(without alignments)
542,450 Million cell updates/sec

Title: US-10-757-863-4
Perfect score: 1169
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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62	1168	99.9	437	5	PCT-US96-10043-11	Sequence 11, Appl
63	1168	99.9	442	4	US-08-472-888A-7	Sequence 7, Appl
64	1168	99.9	442	5	PCT-US96-10043-9	Sequence 9, Appl
65	1168	99.9	446	3	US-08-397-411-7	Sequence 7, Appl
66	1168	99.9	446	4	US-09-157-452B-12	Sequence 12, Appl
67	1168	99.9	449	1	US-08-458-516-13	Sequence 13, Appl
68	1168	99.9	452	4	US-09-773-877B-16	Sequence 16, Appl
69	1168	99.9	455	4	US-09-773-877B-22	Sequence 22, Appl
70	1168	99.9	458	4	US-09-773-877B-26	Sequence 26, Appl
71	1168	99.9	459	1	US-08-157-101A-7	Sequence 7, Appl
72	1168	99.9	462	4	US-09-773-877B-18	Sequence 18, Appl
73	1168	99.9	467	4	US-08-030-175-41	Sequence 41, Appl
74	1168	99.9	467	4	US-08-030-175-42	Sequence 42, Appl
75	1168	99.9	475	4	US-09-740-002-27	Sequence 27, Appl
76	1168	99.9	476	2	US-08-378-939-10	Sequence 10, Appl
77	1168	99.9	476	3	US-08-487-550-4	Sequence 4, Appl
78	1168	99.9	476	3	US-08-487-550-12	Sequence 12, Appl
79	1168	99.9	476	4	US-09-526-098-4	Sequence 4, Appl
80	1168	99.9	476	4	US-09-526-098-12	Sequence 12, Appl
81	1168	99.9	476	4	US-09-526-098-12	Sequence 12, Appl
82	1168	99.9	476	4	US-09-583-916-4	Sequence 4, Appl
83	1168	99.9	476	4	US-09-583-916-12	Sequence 12, Appl
84	1168	99.9	478	3	US-08-487-550-8	Sequence 8, Appl
85	1168	99.9	478	4	US-09-526-098-8	Sequence 8, Appl
86	1168	99.9	478	4	US-09-383-916-8	Sequence 8, Appl
87	1168	99.9	482	3	US-09-189-129-2	Sequence 2, Appl
88	1168	99.9	482	4	US-09-824-286-2	Sequence 2, Appl
89	1168	99.9	488	3	US-08-776-511-2	Sequence 2, Appl
90	1168	99.9	497	4	US-09-469-846-6	Sequence 6, Appl
91	1168	99.9	525	4	US-09-469-846-4	Sequence 4, Appl
92	1168	99.9	547	4	US-09-733-877B-14	Sequence 14, Appl
93	1168	99.9	557	4	US-09-733-877B-14	Sequence 14, Appl
94	1168	99.9	567	4	US-09-823-856A-16	Sequence 16, Appl
95	1168	99.9	567	4	US-09-773-877B-20	Sequence 20, Appl
96	1168	99.9	571	4	US-09-746-359A-53	Sequence 53, Appl
97	1168	99.9	571	4	US-09-313-942-8	Sequence 8, Appl
98	1168	99.9	622	4	US-09-499-846-2	Sequence 2, Appl
99	1168	99.9	680	3	US-08-227-496C-15	Sequence 15, Appl
100	1168	99.9				

101	1168	99.9	691	4	US-09-313-942-20	Sequence 20, Appl
102	1168	99.9	694	4	US-09-313-942-22	Sequence 22, Appl
103	1168	99.9	859	4	US-09-313-942-7	Sequence 7, Appl
104	1168	99.9	951	4	US-09-313-942-9	Sequence 9, Appl
105	1168	99.9	1158	4	US-09-313-942-26	Sequence 26, Appl
106	1168	99.9	1168	4	US-09-313-942-24	Sequence 24, Appl
107	1164	99.6	462	4	US-09-289-942-7	Sequence 7, Appl
108	1164	99.6	475	4	US-09-740-002-25	Sequence 25, Appl
109	1163	99.5	254	2	US-08-284-911-33	Sequence 33, Appl
110	1163	99.5	254	3	US-09-218-950-33	Sequence 33, Appl
111	1163	99.5	254	4	US-08-394-388-33	Sequence 33, Appl
112	1162	99.4	218	4	US-09-483-588-3	Sequence 3, Appl
113	1162	99.4	330	4	US-09-301-593-22	Sequence 22, Appl
114	1162	99.4	397	4	US-08-775-066-2	Sequence 2, Appl
115	1162	99.4	449	3	US-08-897-236-23	Sequence 23, Appl
116	1162	99.4	449	4	US-09-500-253-23	Sequence 23, Appl
117	1162	99.4	450	4	US-09-966-288-208	Sequence 208, Appl
118	1162	99.4	450	4	US-09-966-288-210	Sequence 210, Appl
119	1162	99.4	450	4	US-09-966-288-212	Sequence 212, Appl
120	1162	99.4	450	4	US-09-966-288-214	Sequence 214, Appl
121	1162	99.4	450	4	US-09-966-288-216	Sequence 216, Appl
122	1162	99.4	450	4	US-09-966-288-218	Sequence 218, Appl
123	1162	99.4	450	4	US-09-966-288-220	Sequence 220, Appl
124	1162	99.4	450	4	US-09-966-288-222	Sequence 222, Appl
125	1162	99.4	450	4	US-09-966-288-224	Sequence 224, Appl
126	1162	99.4	450	4	US-09-966-288-226	Sequence 226, Appl
127	1162	99.4	450	4	US-09-966-288-228	Sequence 228, Appl
128	1162	99.4	450	4	US-09-966-288-232	Sequence 232, Appl
129	1162	99.4	450	4	US-09-966-288-234	Sequence 234, Appl
130	1162	99.4	450	4	US-09-966-288-236	Sequence 236, Appl
131	1162	99.4	450	4	US-09-966-288-238	Sequence 238, Appl
132	1162	99.4	450	4	US-09-966-288-240	Sequence 240, Appl
133	1162	99.4	450	4	US-09-966-288-242	Sequence 242, Appl
134	1162	99.4	450	4	US-09-966-288-244	Sequence 244, Appl
135	1162	99.4	450	4	US-09-966-288-246	Sequence 246, Appl
136	1162	99.4	450	4	US-09-966-288-248	Sequence 248, Appl
137	1162	99.4	450	4	US-09-966-288-250	Sequence 250, Appl
138	1162	99.4	450	4	US-09-966-288-252	Sequence 252, Appl
139	1162	99.4	450	4	US-09-966-288-254	Sequence 254, Appl
140	1162	99.4	450	4	US-09-966-288-256	Sequence 256, Appl
141	1162	99.4	451	2	US-08-887-352-14	Sequence 14, Appl
142	1162	99.4	451	2	US-08-887-352-16	Sequence 16, Appl
143	1162	99.4	451	2	US-08-887-352-18	Sequence 18, Appl
144	1162	99.4	451	3	US-08-466-151-65	Sequence 65, Appl
145	1162	99.4	451	3	US-09-109-207C-14	Sequence 14, Appl
146	1162	99.4	451	3	US-09-109-207C-16	Sequence 16, Appl
147	1162	99.4	451	3	US-09-109-207C-18	Sequence 18, Appl
148	1162	99.4	451	3	US-09-282-505-2	Sequence 2, Appl
149	1162	99.4	451	3	US-09-054-235-2	Sequence 2, Appl
150	1162	99.4	451	3	US-09-286-005-14	Sequence 14, Appl

99	1168	99.9	261	7	ABU64198	Abu64198 Plaemid P
100	1168	99.9	261	8	ADO10509	Ado10509 Kb signal
101	1168	99.9	266	5	ABB77128	Abb77128 Human Crl
102	1168	99.9	266	5	ABB77108	Abb77108 Human Crl
103	1168	99.9	266	5	ABB77115	Abb77115 Human Crl
104	1168	99.9	266	5	ABB77121	Abb77121 Human Crl
105	1168	99.9	267	7	AAE26273	AAe26273 Human Crl
106	1168	99.9	267	7	ADK82716	Adk82716 Anti-beta
107	1168	99.9	268	3	AB16959	Ab16959 FC-TMP-TM
108	1168	99.9	268	3	AB16959	Ab16959 FC-TMP-TM
109	1168	99.9	269	3	AA196531	AAy96531 Human IgG
110	1168	99.9	269	3	AB16960	Ab16960 TMP-TMP-F
111	1168	99.9	269	5	ABB73413	Abb73413 TMP-TMP-F
112	1168	99.9	269	8	ADK82719	Adk82719 Anti-beta
113	1168	99.9	277	8	ADJ52120	Adj52120 CHI delet
114	1168	99.9	277	3	AB16967	Ab16967 FC-EMP-EM
115	1168	99.9	277	3	AB16966	Ab16966 EMP-EMP-F
116	1168	99.9	277	5	ABB73418	Abb73418 FC-EMP-EM
117	1168	99.9	277	7	ADR82706	Adr82706 Beta-amy1
118	1168	99.9	281	5	AAE15489	AAe15489 Mouse BCM
119	1168	99.9	281	5	AAU81169	AAu81169 Echistati
120	1168	99.9	283	5	AAE15488	AAe15488 Human BCM
121	1168	99.9	287	4	AAE47590	AAb47590 Fusion pr
122	1168	99.9	293	6	ABJ38345	Abj38345 TALL-1 in
123	1168	99.9	293	6	ABJ38344	Abj38344 TALL-1 in
124	1168	99.9	293	4	ADQ76789	Adq76789 AGP3 pep
125	1168	99.9	302	4	AAE06069	AAe06069 Mouse IgG
126	1168	99.9	302	4	AAE00507	AAe00507 Human BCM
127	1168	99.9	302	7	ADG43717	Adg43717 Human B-c
128	1168	99.9	320	5	AAE22245	AAe22245 Murine Ig
129	1168	99.9	320	6	ABR55865	Ab55865 Human Imm
130	1168	99.9	320	8	ADN49722	Adn49722 Human Imm
131	1168	99.9	329	2	AAE91806	AAe91806 Human Imm
132	1168	99.9	329	8	ADP56389	Adp56389 Human PRO
133	1168	99.9	329	8	ADP56389	Adp56389 Human PRO
134	1168	99.9	330	4	AAE21960	AAe21960 Human IgG
135	1168	99.9	330	4	AAE21960	AAe21960 Human IgG
136	1168	99.9	330	5	AAE21960	AAe21960 Human IgG
137	1168	99.9	330	5	ABR81641	ABr81641 Human IgG
138	1168	99.9	330	5	ABR80576	ABr80576 Human Imm
139	1168	99.9	330	6	ABP71856	ABp71856 Human IgG
140	1168	99.9	330	6	AAE32915	AAe32915 Human Imm
141	1168	99.9	330	6	AAE32627	AAe32627 Human Imm
142	1168	99.9	330	6	ABR82103	ABr82103 Human DR6
143	1168	99.9	330	6	AAO31102	AAo31102 Human A2-
144	1168	99.9	330	6	ABR55836	ABr55836 Anti-Ang-
145	1168	99.9	330	6	AAO30893	AAo30893 Human Imm
146	1168	99.9	330	7	ADF11389	Adf11389 Anti-OPGL
147	1168	99.9	330	7	ADP83605	ADp83605 Cytokine
148	1168	99.9	330	7	ADP83605	ADp83605 Cytokine
149	1168	99.9	330	7	ADF75001	Adf75001 Human Ig
150	1168	99.9	330	8	ADM41537	Adm41537 Anti-inte

ALIGNMENTS

RESULT 1
AAB07475
ID AAB07475 standard; protein; 218 AA.
XX
AC AAB07475;
XX
DT 20-OCT-2000 (first entry)
XX
DE Native IgG Fc region humIgG1 (A allotype).
XX
XX IgG antibody; light chain; Fc region; effector function; cancer; allergy;
KW asthma; LFA-1-mediated disorder; tumour; cancer.
XX
OS Homo sapiens.
XX
FN WO200042072-A2.

XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000WO-US000973.
XX
PR 15-JAN-1999; 99US-0116023P.
XX
PA (GETH) GENENTECH INC.
XX
PI Presta LG;
XX
DR WPI, 2000-476035/41.
XX
PT New Fc region-containing polypeptides that have altered effector function due to one or more amino acid modifications in the Fc region, useful in the treatment of cancer and allergic conditions such as asthma.
XX
PS Disclosure; Fig 22A; 132pp; English.

CC AAB07474-78 represent native IgG Fc regions. The proteins are used to produce Fc region-containing polypeptides that have altered effector function as a consequence of one or more amino acid modifications in the Fc region. The variant polypeptides are useful for treating cancer, allergic conditions such as asthma (with an anti-IgE antibody), and LFA-1 mediated disorders. Where the polypeptide binds the HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a benign or malignant tumour characterized by overexpression of the HER2 receptor. Such cancers include breast cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer.

CC
XX SQ Sequence 218 AA;

Query Match 99.9%; Score 1168; DB 3; Length 218;
Best Local Similarity 99.5%; Pred. No. 1e-87; 1; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 1; Indels 0;

QY 1 PAPELGGPSVFLFPKPKDTLMISRTPEVTCVVADVSHEDPEVKFMYVDGVEVHNAKT 60
DB 1 PAPELGGPSVFLFPKPKDTLMISRTPEVTCVVADVSHEDPEVKFMYVDGVEVHNAKT 60
QY 61 KPREEQYXNTRVSVTLVLDHMDLNGEKYCKSNALPAPLEKTSKAGQPREPOVY 120
DB 61 KPREEQYXNTRVSVTLVLDHMDLNGEKYCKSNALPAPLEKTSKAGQPREPOVY 120
QY 121 TLPPSRDELATNGQSLTCLVGFYPSDIAVWESNGQPENNYKTPVLDSDGSFFLYSK 180
DB 121 TLPPSRDELATNGQSLTCLVGFYPSDIAVWESNGQPENNYKTPVLDSDGSFFLYSK 180
QY 181 LTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 218
DB 181 LTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 218

RESULT 2
AAB76422
ID AAB76422 standard; protein; 218 AA.
XX
AC AAB76422;
XX
DT 10-APR-2001 (first entry)
XX
DE Human IgG1 A allotype Fc region amino acid sequence.
XX
XX Human; erBB2; HER2; cancer; nervous system disease; stroke; ischaemia;
KW metabolic disorder; nutritional deficiency; Alzheimer's disease;
KW Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;
KW Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
XX

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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:26:52 ; Search time 112.5 Seconds
(without alignments)
992.296 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169
Sequence: 1 PABPILGSPVFLFPPKPKD.....MHEALNHNHYOKSLISLSPGK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

1: UniProt_03.*
2: uniprot_sprot.*
3: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.9	348	2	Q6PYX1
2	1168	99.9	473	2	Q6MZV7
3	1168	99.9	478	2	Q6P181
4	1168	99.9	480	2	Q6P181
5	1162	99.4	330	1	GCL_HUMAN
6	1162	99.4	465	2	Q6GMX6
7	1162	99.4	466	2	Q6IN78
8	1162	99.4	469	2	Q7Z7P5
9	1162	99.4	470	2	Q6P184
10	1162	99.4	470	2	Q7Z5W1
11	1162	99.4	472	2	Q6N089
12	1162	99.4	475	2	Q6GMW7
13	1162	99.4	476	2	Q6GMX1
14	1162	99.4	679	2	Q6PQ08
15	1158	99.1	473	2	Q6P055
16	1158	99.1	475	2	Q6MZ06
17	1158	99.1	480	2	Q6N094
18	1158	99.1	481	2	Q6N097
19	1158	99.1	482	2	Q7Z351
20	1157	99.0	487	2	Q6S2L2
21	1155	98.8	466	2	Q6N096
22	1151	98.5	475	2	Q6N095
23	1151	98.5	544	2	Q6P185
24	1124	96.2	354	2	Q6BT12
25	1124	96.2	518	2	Q6N030
26	1120	95.8	521	2	Q6N4Y9
27	1113	95.2	327	1	GCL_HUMAN
28	1113	95.2	473	1	Q6TFC3
29	1112.5	95.2	326	1	GCL_HUMAN
30	1112.5	95.2	417	2	Q6N093
31	1109.5	94.9	464	2	Q6MZ06

32	1109	94.9	509	2	Q6N177	Q6N177	homo sapien
33	1107.5	94.7	465	2	Q6P6C4	Q6P6C4	homo sapien
34	1104	94.4	250	1	GCB_HUMAN	GCB_HUMAN	homo sapien
35	1104	94.4	476	2	Q6MZT7	Q6MZT7	homo sapien
36	1098.5	94.0	493	2	Q68CN4	Q68CN4	homo sapien
37	893	76.4	333	1	GC_RABIT	GC_RABIT	homo sapien
38	875	74.9	337	2	Q65M34	Q65M34	equus caball
39	853	73.0	339	1	G62_CAVPO	G62_CAVPO	cavia porce
40	836	71.5	339	1	GC3_MOUSE	GC3_MOUSE	mus musculus
41	836	71.5	470	2	Q7TMK1	Q7TMK1	mus musculus
42	825	70.6	303	2	Q6KAM2	Q6KAM2	mus musculus
43	825	70.6	398	1	GC3M_MOUSE	GC3M_MOUSE	mus musculus
44	818.5	70.0	453	2	Q991C4	Q991C4	mus musculus
45	817.5	69.9	458	2	Q65ZQ1	Q65ZQ1	homo sapien
46	816	69.8	326	1	GCL_RAT	GCL_RAT	rattus norv
47	815	69.7	333	1	GCB_RAT	GCB_RAT	rattus norv
48	807.5	69.1	334	1	GCL_MOUSE	GCL_MOUSE	rattus norv
49	805	68.9	339	1	GCC_RAT	GCC_RAT	rattus norv
50	802.5	68.6	333	1	GCL_MOUSE	GCL_MOUSE	rattus norv
51	790	67.6	330	1	GCA_MOUSE	GCA_MOUSE	mus musculus
52	790	67.6	464	2	Q6P185	Q6P185	mus musculus
53	786	67.2	464	2	Q6P188	Q6P188	mus musculus
54	786	67.2	465	2	Q6P182	Q6P182	mus musculus
55	786	67.2	471	2	Q6K04	Q6K04	mus musculus
56	786	67.2	472	2	Q6P187	Q6P187	mus musculus
57	785	67.2	339	1	GCA_MOUSE	GCA_MOUSE	mus musculus
58	784	67.1	332	1	GCA_RAT	GCA_RAT	rattus norv
59	782	66.9	335	1	GCB_MOUSE	GCB_MOUSE	mus musculus
60	782	66.9	433	2	Q9DB14	Q9DB14	mus musculus
61	758	64.8	473	2	Q91Z05	Q91Z05	mus musculus
62	758	64.8	474	2	Q8R3H6	Q8R3H6	mus musculus
63	757	64.8	336	1	GCB_MOUSE	GCB_MOUSE	mus musculus
64	752	64.3	405	1	GCB_MOUSE	GCB_MOUSE	mus musculus
65	358	30.6	375	2	Q86T11	Q86T11	homo sapien
66	358	30.6	454	1	MUC_HUMAN	MUC_HUMAN	homo sapien
67	358	30.6	597	2	Q6EBB9	Q6EBB9	homo sapien
68	358	30.6	597	2	Q6GMX5	Q6GMX5	homo sapien
69	358	30.6	597	2	Q9BQ08	Q9BQ08	homo sapien
70	358	30.6	597	2	Q9B101	Q9B101	homo sapien
71	358	30.6	606	2	Q6GMV2	Q6GMV2	homo sapien
72	356	30.5	391	1	MUCB_HUMAN	MUCB_HUMAN	homo sapien
73	355	30.4	429	1	EPC_RAT	EPC_RAT	rattus norv
74	354.5	30.3	585	2	Q6GFX4	Q6GFX4	xenopus lae
75	354	30.3	421	1	EPC_MOUSE	EPC_MOUSE	mus musculus
76	348.5	29.8	584	2	Q6INK3	Q6INK3	xenopus lae
77	348	29.8	595	2	Q6WUX4	Q6WUX4	homo sapien
78	348	29.8	613	2	Q8WTK1	Q8WTK1	homo sapien
79	348	29.8	620	2	Q96EY0	Q96EY0	homo sapien
80	348	29.8	625	2	Q96A46	Q96A46	homo sapien
81	346	29.6	455	1	MUC_MOUSE	MUC_MOUSE	mus musculus
82	344	29.4	428	1	BPC_HUMAN	BPC_HUMAN	homo sapien
83	338	28.9	614	2	Q7TWT6	Q7TWT6	mus musculus
84	336	28.7	458	1	MUC_RABIT	MUC_RABIT	mus musculus
85	336	28.7	476	1	MUC_MOUSE	MUC_MOUSE	mus musculus
86	336	28.7	613	2	Q8VXC7	Q8VXC7	mus musculus
87	332	28.4	450	1	MUC_CANFA	MUC_CANFA	canis fami
88	325	27.9	479	1	MUC_RABIT	MUC_RABIT	mus musculus
89	325	27.8	454	1	MUC_MESAU	MUC_MESAU	mesocricetus
90	325	27.6	457	1	MUC_SUNMU	MUC_SUNMU	suncus muri
91	316	27.0	572	2	Q66107	Q66107	xenopus lae
92	313	26.8	587	2	Q7TOR1	Q7TOR1	xenopus lae
93	313	26.8	588	2	Q6IR66	Q6IR66	xenopus lae
94	313	26.8	593	2	Q6INM5	Q6INM5	xenopus lae
95	313	26.8	605	2	Q6GN83	Q6GN83	xenopus lae
96	307	26.3	614	2	Q6DD07	Q6DD07	xenopus lae
97	291	24.9	438	1	HVC2_HETFR	HVC2_HETFR	heterodontu
98	287.5	23.6	446	1	MUC_CHICK	MUC_CHICK	gallus gall
99	278.5	23.6	299	1	ALC_RABIT	ALC_RABIT	oryctolagus
100	278	23.8	438	1	HVC1_HETFR	HVC1_HETFR	heterodontu
101	274	23.4	370	1	HVC1_HETFR	HVC1_HETFR	heterodontu
102	269	23.0	461	1	HVC2_HETFR	HVC2_HETFR	heterodontu
103	267	22.8	393	1	HVC1_HETFR	HVC1_HETFR	heterodontu
104	263.5	22.5	684	2	Q90544	Q90544	ginglymосто


```
105 258.5 22.1 478 2 Q72379 Q72379 homo sapien
106 258.5 22.1 492 2 Q72374 Q72374 homo sapien
107 256.5 21.9 340 1 ALC2_HUMAN ALC2_HUMAN
108 256.5 21.9 416 2 Q9NP6 Q9NP6 homo sapien
109 256.5 21.9 477 2 Q6GMX7 Q6GMX7 homo sapien
110 256.5 21.9 478 2 Q6NYH3 Q6NYH3 homo sapien
111 256.5 21.9 479 2 Q6MZV6 Q6MZV6 homo sapien
112 256.5 21.9 480 2 Q6P089 Q6P089 homo sapien
113 256.5 21.9 483 2 Q6MZ9 Q6MZ9 homo sapien
114 256.5 21.9 487 2 Q6ZX0 Q6ZX0 homo sapien
115 256 21.9 353 1 ALC1_HUMAN ALC1_HUMAN
116 256 21.9 384 2 Q9UP6 Q9UP6 homo sapien
117 256 21.9 493 2 Q8NCL6 Q8NCL6 homo sapien
118 256 21.9 493 2 Q6GMX2 Q6GMX2 homo sapien
119 256 21.9 494 2 Q6K68 Q6K68 homo sapien
120 256 21.9 496 2 Q6KX8 Q6KX8 homo sapien
121 256 21.9 506 2 Q6MZ0 Q6MZ0 homo sapien
122 256 21.9 506 2 Q6N090 Q6N090 homo sapien
123 255.5 21.9 498 2 Q6N041 Q6N041 homo sapien
124 255.5 21.9 500 2 Q6N091 Q6N091 homo sapien
125 254.5 21.8 353 1 ALC1_GORGO ALC1_GORGO
126 253 21.6 494 2 Q6ZM64 Q6ZM64 homo sapien
127 253 21.6 496 2 Q6DK0 Q6DK0 homo sapien
128 253 21.6 499 2 Q8NSK4 Q8NSK4 homo sapien
129 253 21.6 519 2 Q6N092 Q6N092 homo sapien
130 251 21.5 497 2 Q8WY24 Q8WY24 homo sapien
131 251 21.5 500 2 Q6BRV0 Q6BRV0 homo sapien
132 246.5 21.1 481 1 MUCM ICTPU MUCM ICTPU
133 246.5 20.7 481 2 Q91WT1 Q91WT1 mus musculus
134 242.5 20.7 481 2 Q91WT3 Q91WT3 mus musculus
135 242.5 20.7 482 2 Q91X92 Q91X92 mus musculus
136 242.5 20.7 482 2 Q8K172 Q8K172 mus musculus
137 242.5 20.7 484 2 Q8VEA0 Q8VEA0 mus musculus
138 242.5 20.7 485 2 Q6PDB8 Q6PDB8 mus musculus
139 242.5 20.7 487 2 Q80Z17 Q80Z17 mus musculus
140 242.5 20.7 488 2 Q8K0F2 Q8K0F2 mus musculus
141 242.5 20.7 488 2 Q91MR1 Q91MR1 mus musculus
142 240.5 20.7 489 2 Q8VXC4 Q8VXC4 mus musculus
143 240.5 20.6 479 2 Q91WP5 Q91WP5 mus musculus
144 239.5 20.5 344 1 ALC_MOUSE ALC_MOUSE
145 239.5 20.5 479 2 Q9NM22 Q9NM22 mus musculus
146 239.5 20.5 479 2 Q7TMK4 Q7TMK4 mus musculus
147 239.5 20.5 480 2 Q91XE1 Q91XE1 mus musculus
148 239.5 20.5 480 2 Q8K0Z4 Q8K0Z4 mus musculus
149 239.5 20.5 481 2 Q8VCV5 Q8VCV5 mus musculus
150 239.5 20.5 484 2 Q99LAE Q99LAE mus musculus
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ALIGNMENTS

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RESULT 1
ID Q6PYX1 PRELIMINARY; PRT; 348 AA.
AC Q6PYX1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hepatitis B virus receptor binding protein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhu N.S., Chen Y.Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570731; AAS88328.1; -.
DR HSSP; P01857; IAD7.
DR GO; GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
```

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DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Receptor.
FT NON_TER
SQ SEQUENCE 348 AA; 38162 MW; DD96C3D7E0BE5845 CRC64;
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Query Match 99.9%; Score 1168; DB 2; Length 348;
Best Local Similarity 99.5%; Pred. No. 2.7e-87;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 PAPERLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 60
Db 131 PAPERLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 190
Qy 61 KPREQYNYTYRVVSVLTVLHQMNLNGEKYCKVSNKALPAPIKTSKAKGPREPOVY 120
Db 191 KPREQYNYTYRVVSVLTVLHQMNLNGEKYCKVSNKALPAPIKTSKAKGPREPOVY 250
Qy 121 TLPPSRREMTNQVSLTCLVNGFYPSDIAVWESNGQEPENNYKTPPLVDSGSFFLYSK 180
Db 251 TLPPSRREMTNQVSLTCLVNGFYPSDIAVWESNGQEPENNYKTPPLVDSGSFFLYSK 310
Qy 181 LTVDSKRWQGNVFSQVMEALHNHYTKSLSPGK 218
Db 311 LTVDSKRWQGNVFSQVMEALHNHYTKSLSPGK 348
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RESULT 2

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ID Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA The German Human small intestine;
RG Bloecher H., Boecher M., Nemes H.W., Weil B., Amid C., Osanger A.,
RA Fodor G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAB45920.1; -.
DR HSSP; P01861; IAD0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00407; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;
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Query Match 99.9%; Score 1168; DB 2; Length 473;
Best Local Similarity 99.5%; Pred. No. 3.9e-87;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 PAPERLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 60
Db 256 PAPERLGGPSVFLPPPKKDTLMSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 315
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:31:08 ; Search time 25 Seconds

(without alignments)
839,010 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169
Sequence: 1 PABPLLGGPSVFLPPPKPKD.....MREALNNHYTKSLSLSPGK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.9	374	2 S69339	Ig heavy chain V r
2	1162	99.4	255	4 S31866	Ig gamma-1 chain C
3	1162	99.4	330	1 GHMV	Ig gamma-1 chain C
4	1124	96.2	377	2 A23511	Ig gamma-3 chain C
5	1122	96.0	377	2 A60764	Ig gamma-3 chain C
6	1116	95.5	234	1 PT0207	Ig gamma-4 chain C
7	1113	95.2	327	1 G4HV	Ig gamma-4 chain C
8	1112.5	95.2	326	1 G2HV	Ig gamma-2 chain C
9	1099	94.0	289	1 G3HVI	Ig gamma-3 heavy C
10	893	76.4	323	1 GHRB	Ig gamma chain C r
11	883	75.5	328	2 I47160	Ig gamma-2 chain
12	883	75.5	328	2 I47159	Ig gamma 2a chain
13	877	75.0	277	2 I47162	Ig gamma 4 chain c
14	857	73.3	328	2 I47158	Ig gamma 1 chain c
15	855	73.1	328	2 I47161	Ig gamma 3 chain c
16	836	73.0	329	1 G2GP	Ig gamma-2 chain C
17	836	71.5	329	1 G3MSC	Ig gamma-3 chain C
18	836	71.5	470	2 S22080	Ig heavy chain pre
19	832	71.2	308	2 C30554	Ig heavy chain C r
20	832	71.2	472	2 S31459	Ig gamma-1 chain c
21	825	70.6	368	1 G3NSM	Ig gamma-3 chain C
22	817.5	69.9	444	2 PC4436	monoclonal antibody
23	816	69.8	326	2 PS0017	Ig gamma-1 chain C
24	815	69.7	324	2 PS0018	Ig gamma-2b chain
25	807.5	69.1	329	1 G1MS	Ig gamma-1 chain C
26	806	68.9	334	2 S00847	Ig gamma-2c chain
27	802.5	68.6	393	1 G1NSM	Ig gamma-1 chain C
28	790	67.6	330	1 G2MSA	Ig gamma-2a chain
29	790	67.6	469	2 S37483	Ig gamma-2a chain

30	785	67.2	399	1 G2MSAM	Ig gamma-2a chain
31	784	67.1	332	2 PS0019	Ig gamma-2a chain
32	782	66.9	325	1 G2MSAB	Ig gamma-2a chain
33	775	66.3	446	2 S40295	Ig gamma-2a chain
34	761	65.1	327	2 S06611	Ig gamma-2 chain C
35	757	64.8	474	1 G2MS11	Ig gamma-2b chain
36	752	64.3	405	1 G2MSBM	Ig gamma-2b chain
37	735	62.9	475	2 S01321	Ig gamma-2b chain
38	704	60.2	180	2 I46732	Ig gamma heavy cha
39	582.5	49.8	249	2 S69340	Ig heavy chain VHI
40	573	49.0	152	2 S14236	Ig gamma-1 chain C
41	568.5	48.6	218	2 A36040	Ig heavy chain V-I
42	395	33.8	572	2 B46529	Ig y heavy chain (
43	358	30.6	453	3 S37768	Ig mu chain C regi
44	356	30.5	391	1 MHHUBT	Ig mu heavy chain
45	355.5	30.4	448	2 S03186	Ig heavy chain C r
46	355	30.4	429	1 EHRT	Ig epsilon chain C
47	354	30.3	388	1 EHMS	Ig epsilon chain C
48	351	30.0	548	2 S38864	Ig epsilon chain C
49	350.5	30.0	549	2 S04845	Ig heavy chain pre
50	349.5	29.9	452	1 MHRU	Ig mu chain C regi
51	348	29.8	627	2 S14683	Ig mu chain precu
52	347	29.7	343	2 S25644	Ig mu chain C regi
53	346	29.6	455	1 MHMS	Ig mu chain C regi
54	346	29.6	455	2 A24976	Ig mu chain C regi
55	345	29.5	426	2 I36948	Ig epsilon-chain -
56	345	29.5	474	2 S15590	Ig heavy chain - h
57	344	29.4	428	1 EHRU	Ig epsilon chain C
58	339.5	29.0	473	1 MHRUM	Ig mu chain C regi
59	337.5	28.9	504	2 S00390	Ig gamma chain (c1
60	336	28.7	458	1 MHRB	Ig mu chain C regi
61	336	28.7	476	1 MHRSM	Ig mu chain C regi
62	332.5	28.4	423	1 EHMSS	Ig epsilon chain C
63	332	28.4	450	1 MHDC	Ig mu chain C regi
64	328	28.1	454	1 MHRY	Ig mu chain C regi
65	327.5	28.0	112	2 B30503	Ig gamma-2a chain
66	326	27.9	479	1 MHRBM	Ig mu chain C regi
67	323	27.6	457	2 S03961	Ig mu chain C regi
68	322	27.5	592	2 S25705	Ig mu chain - bhee
69	313	26.8	453	2 C31933	Ig mu chain C regi
70	296	25.3	577	2 I50731	Ig heavy chain - n
71	295.5	25.3	433	2 S31436	Ig epsilon chain -
72	291	24.9	438	1 HVRK2	Ig mu chain C regi
73	289.5	24.8	342	2 I47175	Ig alpha chain C r
74	287.5	24.6	367	1 MHCH	Ig mu chain C regi
75	278.5	23.8	299	1 AHRB	Ig alpha chain C r
76	278	23.8	343	2 S09272	Ig mu chain C regi
77	278	23.8	438	1 HVRKCS	Ig mu chain C regi
78	274	23.4	370	1 HVRKS5	Ig mu chain C regi
79	273.5	23.4	585	2 A46507	Ig alpha chain - c
80	272.5	23.3	338	2 S09276	Ig alpha chain C r
81	271.5	23.2	88	2 A30503	Ig gamma-2b chain
82	269	23.0	461	1 HVRKCO	Ig mu chain C regi
83	268.5	23.0	339	2 S09264	Ig alpha chain C r
84	267	22.8	357	2 S09269	Ig mu chain C regi
85	267	22.8	393	1 HVRK1	Ig heavy chain C r
86	263.5	22.5	244	2 S12328	Ig heavy chain C r
87	263.5	22.5	684	2 S60266	novel antigen rece
88	263	22.5	111	2 S43148	Ig epsilon chain -
89	261.5	22.4	357	2 S09265	Ig alpha chain C r
90	259.5	22.2	348	2 S09270	Ig alpha chain C r
91	259.5	22.2	352	2 S09266	Ig mu chain C r
92	257.5	22.0	474	2 I50830	Ig mu chain - lepi
93	256.5	21.9	340	2 I56230	Ig alpha-2 chain -
94	256.5	21.9	340	2 B23360	Ig alpha-2 chain C
95	256.5	21.9	347	2 S09274	Ig alpha chain C r
96	256	21.9	353	1 AHRU	Ig alpha chain C r
97	254.5	21.8	352	2 S05500	Ig alpha-1 chain C
98	253.5	21.7	454	2 A46532	Ig mu chain C regi
99	253	21.6	360	2 S09271	Ig alpha chain C r
100	253	21.6	568	2 A34891	Ig heavy chain pre
101	250.5	21.4	348	2 S09273	Ig alpha chain C r
102	247.5	21.2	340	1 A2HU	Ig alpha-2 chain C

103 247 21.1 342 2 A45966 Ig alpha chain C r
104 246.5 21.1 568 2 A45804 Ig mu chain C regi
105 246 21.0 220 2 C22360 Ig lambda-2 chain C
106 246 21.0 357 2 S09267 Ig alpha chain C r
107 245 21.0 573 2 S12838 Ig mu chain precu
108 239.5 19.8 344 1 AHMS Ig alpha chain C r
109 231.5 19.8 335 2 S09275 Ig alpha chain C r
110 231 19.8 580 2 A46538 Ig heavy chain, se
111 227 19.4 358 2 S09268 Ig alpha chain C r
112 212 18.1 115 2 I68731 IGE chain C4 regio
113 209 17.9 448 2 A46533 Ig heavy chain C r
114 206 17.6 402 2 S20002 Ig heavy chain, se
115 205 17.5 115 2 I68727 IGE chain C4 regio
116 202 17.3 228 2 S03050 Ig gamma chain C1
117 186.5 16.0 140 2 A34509 Ig light chain C r
118 184.5 15.8 106 2 S22760 Ig lambda-2 chain
119 184.5 15.8 214 2 PC4156 Ig lambda chain V
120 183 15.7 212 2 S70431 Ig lambda chain -
121 181 15.5 231 2 S25751 Ig heavy chain -
122 181 15.5 1005 2 T18537 Ig heavy chain - c
123 180 15.4 216 2 S03401 SHP substrate-1 pr
124 180 15.4 509 2 JCS288 SHP substrate-1 pr
125 180 15.4 513 2 UCS289 SHP substrate-1 pr
126 179.5 15.4 233 2 I51383 Ig lambda chain -
127 179.5 15.4 240 2 A41797 Ig light chain - s
128 179 15.3 105 2 B27390 Ig lambda-1 chain
129 178.5 15.3 105 1 LIMS Ig lambda-2 chain
130 178 15.2 118 2 A46516 Ig lambda chain C
131 176 15.1 102 2 B34509 Ig light chain C r
132 176 15.1 118 2 A39949 Ig lambda chain J-
133 175 15.0 227 2 PH1215 Ig epsilon chain C
134 175 15.0 243 2 PH1216 Ig epsilon chain C
135 174 14.9 232 2 S25756 Ig lambda chain -
136 174 14.9 235 2 S25750 Ig lambda chain -
137 173 14.8 118 2 C46516 Ig lambda chain C
138 172 14.7 118 2 S12440 Ig lambda chain (M
139 172 14.7 235 2 S25754 Ig lambda chain -
140 172 14.7 235 2 S25758 Ig lambda chain -
141 171.5 14.7 118 2 B30505 Ig lambda-6 chain
142 171.5 14.7 232 2 S17399 Ig lambda chain pr
143 171 14.6 118 2 S12443 Ig lambda chain (K
144 170 14.5 105 2 S27632 Ig lambda-2 chain
145 170 14.5 231 2 S25738 Ig lambda chain -
146 169.5 14.5 234 2 S25757 Ig lambda chain -
147 169 14.5 115 2 E53116 Ig epsilon chain C
148 169 14.5 235 2 S05270 Ig lambda chain pr
149 168.5 14.4 231 2 PC4155 Ig gamma-2b chain
150 168 14.4 105 2 S22759 Ig lambda-2 chain

ALIGNMENTS

RESULT 1
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khanlich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687; PMID:7744049
A:Accession: S69339
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khanlich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 99.9%; Score 1168; DB 2; Length 374;
Best Local Similarity 99.5%; Pred. No. 5.8e-86;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PAPELLGSPVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 60
DB 157 PAPELLGSPVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 216
QY 61 KPREQYNKYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 120
DB 217 KPREQYNKYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 276
QY 121 TLPPSRREMTKNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 180
DB 277 TLPPSRREMTKNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 336
QY 181 LTVDKSRWQOGNVSFCSYMEHALNHYTKSLSPCK 218
DB 337 LTVDKSRWQOGNVSFCSYMEHALNHYTKSLSPCK 374

RESULT 2

S31866
Ig gamma-1 chain C region - synthetic

C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C>Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.

A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FTL>
A:Cross-references: EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:G33069
C:Keywords: Immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 99.4%; Score 1162; DB 4; Length 255;
Best Local Similarity 98.6%; Pred. No. 1.1e-85;
Matches 215; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PAPELLGSPVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 60
DB 38 PAPELLGSPVFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFMNYVDGVEVHNAKT 97
QY 61 KPREQYNKYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 120
DB 98 KPREQYNKYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 157
QY 121 TLPPSRREMTKNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 180
DB 158 TLPPSRREMTKNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSK 217
QY 181 LTVDKSRWQOGNVSFCSYMEHALNHYTKSLSPCK 218
DB 218 LTVDKSRWQOGNVSFCSYMEHALNHYTKSLSPCK 255

RESULT 3

GHNU
Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)
C>Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S36861; S38887; B90563; A90564; B91668; A91723; A02146
R:Elison, J.W.; Berson, B.J.; Hood, L.E.

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OM protein - protein search, using SW model

Run on: September 22, 2005, 12:58:35 ; Search time 60.5 Seconds
(without alignments)
1466.589 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169

Sequence: 1 PAPERLOGPSVFLPPPKKD.....MHEALHNYTKSLSLSPGK 218

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 150 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1168	99.9	218	9	US-09-813-341-1
2	1168	99.9	218	14	US-10-277-370-1
3	1168	99.9	218	15	US-10-196-394-72
4	1168	99.9	218	15	US-10-370-749-15
5	1168	99.9	218	16	US-10-835-642-3
6	1168	99.9	218	16	US-10-757-863-3
7	1168	99.9	218	17	US-10-982-470-3
8	1168	99.9	223	14	US-10-135-636-3
9	1168	99.9	228	17	US-10-399-093-5
10	1168	99.9	232	9	US-09-977-034-4
11	1168	99.9	232	14	US-10-071-459A-15

12	1168	99.9	232	14	US-10-292-418-2	Sequence 2, Appli
13	1168	99.9	232	14	US-10-020-354-83	Sequence 83, Appli
14	1168	99.9	232	15	US-10-466-593-2	Sequence 2, Appli
15	1168	99.9	232	15	US-10-419-058-6	Sequence 6, Appli
16	1168	99.9	232	17	US-10-953-259-4	Sequence 4, Appli
17	1168	99.9	264	15	US-10-433-108-18	Sequence 18, Appli
18	1168	99.9	264	15	US-10-433-108-20	Sequence 20, Appli
19	1168	99.9	272	15	US-10-433-108-19	Sequence 19, Appli
20	1168	99.9	272	15	US-10-433-108-21	Sequence 21, Appli
21	1168	99.9	272	15	US-10-433-108-22	Sequence 22, Appli
22	1168	99.9	272	15	US-10-433-108-29	Sequence 29, Appli
23	1168	99.9	272	15	US-10-433-108-30	Sequence 30, Appli
24	1168	99.9	280	15	US-10-433-108-27	Sequence 27, Appli
25	1168	99.9	287	15	US-10-433-108-23	Sequence 28, Appli
26	1168	99.9	287	15	US-10-433-108-28	Sequence 28, Appli
27	1168	99.9	287	15	US-10-433-108-31	Sequence 31, Appli
28	1168	99.9	294	15	US-10-433-108-26	Sequence 26, Appli
29	1168	99.9	302	15	US-10-433-108-25	Sequence 25, Appli
30	1168	99.9	329	15	US-10-370-749-25	Sequence 25, Appli
31	1168	99.9	329	16	US-10-426-334-1	Sequence 1, Appli
32	1168	99.9	330	9	US-09-301-593-22	Sequence 22, Appli
33	1168	99.9	330	14	US-10-121-464-20	Sequence 20, Appli
34	1168	99.9	330	14	US-10-159-006-22	Sequence 22, Appli
35	1168	99.9	330	15	US-10-366-709-52	Sequence 52, Appli
36	1168	99.9	330	16	US-10-688-925-53	Sequence 53, Appli
37	1168	99.9	330	16	US-10-741-481-45	Sequence 45, Appli
38	1168	99.9	330	17	US-10-901-735-3	Sequence 3, Appli
39	1168	99.9	330	17	US-10-706-689-2	Sequence 2, Appli
40	1168	99.9	330	18	US-10-988-360-2	Sequence 2, Appli
41	1168	99.9	334	16	US-10-424-986-28	Sequence 28, Appli
42	1168	99.9	367	16	US-10-424-986-26	Sequence 26, Appli
43	1168	99.9	397	8	US-08-779-457-47	Sequence 47, Appli
44	1168	99.9	397	17	US-10-921-710-47	Sequence 4, Appli
45	1168	99.9	397	17	US-10-491-997-16	Sequence 16, Appli
46	1168	99.9	399	9	US-09-859-361-7	Sequence 7, Appli
47	1168	99.9	401	9	US-09-854-280-12	Sequence 12, Appli
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55	1168	99.9	449	14	US-10-323-268-23	Sequence 23, Appli
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68	1168	99.9	450	9	US-09-996-288-210	Sequence 210, Appli
69	1168	99.9	450	9	US-09-996-288-212	Sequence 212, Appli
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71	1168	99.9	450	9	US-09-996-288-216	Sequence 216, Appli
72	1168	99.9	450	9	US-09-996-288-218	Sequence 218, Appli
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83	1168	99.9	450	9	US-09-996-288-242	Sequence 242, Appli
84	1168	99.9	450	9	US-09-996-288-242	Sequence 242, Appli

85	1168	99.9	450	9	US-09-996-288-244	Sequence 244, App
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87	1168	99.9	450	9	US-09-996-288-248	Sequence 248, App
88	1168	99.9	450	9	US-09-996-288-250	Sequence 250, App
89	1168	99.9	450	9	US-09-996-288-252	Sequence 252, App
90	1168	99.9	450	9	US-09-996-288-254	Sequence 254, App
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92	1168	99.9	450	10	US-09-996-285-208	Sequence 208, App
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100	1168	99.9	450	10	US-09-996-285-224	Sequence 224, App
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102	1168	99.9	450	10	US-09-996-285-228	Sequence 228, App
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106	1168	99.9	450	10	US-09-996-285-238	Sequence 238, App
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115	1168	99.9	450	10	US-09-996-285-256	Sequence 256, App
116	1168	99.9	450	14	US-10-135-636-1	Sequence 1, Appli
117	1168	99.9	450	17	US-10-900-230-208	Sequence 208, App
118	1168	99.9	450	17	US-10-900-230-210	Sequence 210, App
119	1168	99.9	450	17	US-10-900-230-212	Sequence 212, App
120	1168	99.9	450	17	US-10-900-230-214	Sequence 214, App
121	1168	99.9	450	17	US-10-900-230-216	Sequence 216, App
122	1168	99.9	450	17	US-10-900-230-218	Sequence 218, App
123	1168	99.9	450	17	US-10-900-230-220	Sequence 220, App
124	1168	99.9	450	17	US-10-900-230-222	Sequence 222, App
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126	1168	99.9	450	17	US-10-900-230-226	Sequence 226, App
127	1168	99.9	450	17	US-10-900-230-228	Sequence 228, App
128	1168	99.9	450	17	US-10-900-230-232	Sequence 232, App
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139	1168	99.9	450	17	US-10-900-230-254	Sequence 254, App
140	1168	99.9	450	17	US-10-900-230-256	Sequence 256, App
141	1168	99.9	450	18	US-10-962-285-208	Sequence 208, App
142	1168	99.9	450	18	US-10-962-285-210	Sequence 210, App
143	1168	99.9	450	18	US-10-962-285-212	Sequence 212, App
144	1168	99.9	450	18	US-10-962-285-214	Sequence 214, App
145	1168	99.9	450	18	US-10-962-285-216	Sequence 216, App
146	1168	99.9	450	18	US-10-962-285-218	Sequence 218, App
147	1168	99.9	450	18	US-10-962-285-220	Sequence 220, App
148	1168	99.9	450	18	US-10-962-285-222	Sequence 222, App
149	1168	99.9	450	18	US-10-962-285-224	Sequence 224, App
150	1168	99.9	450	18	US-10-962-285-226	Sequence 226, App

ALIGNMENTS

RESULT 1
US-09-813-341-1

Qy	1	PAPBLLGSPSVFLPFPKXKDTLMISRPEVTCVVVDVSHEDPEVKFNMTYDGVVHNAKT	60	Sequence 1, Application US/09813341
Db	1	PAPBLLGSPSVFLPFPKXKDTLMISRPEVTCVVVDVSHEDPEVKFNMTYDGVVHNAKT	60	Publication No. US20020004587A1
Qy	61	KPREQVXKTYRNVSVLTVLHODMNGEKYCKVSNKALPAPIETKTSKAGQPREPOVY	120	GENERAL INFORMATION:
Db	61	KPREQVXKTYRNVSVLTVLHODMNGEKYCKVSNKALPAPIETKTSKAGQPREPOVY	120	APPLICANT: Miller, Kathy L.
Qy	121	TLPSREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQEPENNYKTTTPVLDSGSPFLYSK	180	APPLICANT: Presta, Leonard G.
Db	121	TLPSREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQEPENNYKTTTPVLDSGSPFLYSK	180	FILE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREFOR
Qy	181	LTVDKSRWQGNVSVCSVMHEALNNHYTKSLSPGK	218	FILE REFERENCE: P1780R1
Db	181	LTVDKSRWQGNVSVCSVMHEALNNHYTKSLSPGK	218	CURRENT APPLICATION NUMBER: US/09/813.341
Qy	217	Conservative	0	PRIOR FILING DATE: 2001-03-20
Db	217	Conservative	0	PRIOR APPLICATION NUMBER: US 60/195,819
Qy	218	Length: 218	0	PRIOR FILING DATE: 2000-04-11
Db	218	Length: 218	0	NUMBER OF SEQ ID NOS: 11
Qy	219	Organism: Homo sapiens	0	SEQ ID NO 1
Db	219	Organism: Homo sapiens	0	TYPE: PRT
Qy	220	Query Match	99.9%; Score 1168; DB 9; Length 218;	US-09-813-341-1
Db	220	Best Local Similarity	99.5%; Pred. No. 6e-89; 1; Indels 0; Gaps 0;	
Qy	221	Matches	217; Conservative	
Db	221	Matches	217; Conservative	
Qy	61	KPREQVXKTYRNVSVLTVLHODMNGEKYCKVSNKALPAPIETKTSKAGQPREPOVY	120	
Db	61	KPREQVXKTYRNVSVLTVLHODMNGEKYCKVSNKALPAPIETKTSKAGQPREPOVY	120	
Qy	121	TLPSREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQEPENNYKTTTPVLDSGSPFLYSK	180	
Db	121	TLPSREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQEPENNYKTTTPVLDSGSPFLYSK	180	
Qy	181	LTVDKSRWQGNVSVCSVMHEALNNHYTKSLSPGK	218	
Db	181	LTVDKSRWQGNVSVCSVMHEALNNHYTKSLSPGK	218	
Qy	217	Conservative	0	
Db	217	Conservative	0	
Qy	218	Length: 218	0	
Db	218	Length: 218	0	
Qy	219	Organism: homo sapiens	0	
Db	219	Organism: homo sapiens	0	
Qy	220	Query Match	99.9%; Score 1168; DB 14; Length 218;	
Db	220	Best Local Similarity	99.5%; Pred. No. 6e-89; 1; Indels 0; Gaps 0;	
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Db	221	Matches	217; Conservative	
Qy	61	KPREQVXKTYRNVSVLTVLHODMNGEKYCKVSNKALPAPIETKTSKAGQPREPOVY	120	
Db	61	KPREQVXKTYRNVSVLTVLHODMNGEKYCKVSNKALPAPIETKTSKAGQPREPOVY	120	
Qy	121	TLPSREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQEPENNYKTTTPVLDSGSPFLYSK	180	
Db	121	TLPSREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQEPENNYKTTTPVLDSGSPFLYSK	180	

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OM protein - protein search, using SW model

Run on: September 22, 2005, 12:35:38 / Search time 30 Seconds
(without alignments)
542.450 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169

Sequence: 1 PABELLGSPSEVFLPPKPKD.....MREALNHNYTKSLSPGK 218

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74643064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database:

Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1168	99.9	218	4	US-09-483-588-3	Sequence 3, Appl
2	1168	99.9	330	4	US-09-301-593-22	Sequence 22, Appl
3	1168	99.9	397	4	US-08-775-066-2	Sequence 2, Appl
4	1168	99.9	449	3	US-08-897-236-23	Sequence 23, Appl
5	1168	99.9	449	4	US-09-500-2538-23	Sequence 23, Appl
6	1168	99.9	450	4	US-09-986-288-208	Sequence 208, Appl
7	1168	99.9	450	4	US-09-986-288-210	Sequence 210, Appl
8	1168	99.9	450	4	US-09-986-288-212	Sequence 212, Appl
9	1168	99.9	450	4	US-09-986-288-214	Sequence 214, Appl
10	1168	99.9	450	4	US-09-986-288-216	Sequence 216, Appl
11	1168	99.9	450	4	US-09-986-288-218	Sequence 218, Appl
12	1168	99.9	450	4	US-09-986-288-220	Sequence 220, Appl
13	1168	99.9	450	4	US-09-986-288-222	Sequence 222, Appl
14	1168	99.9	450	4	US-09-986-288-224	Sequence 224, Appl
15	1168	99.9	450	4	US-09-986-288-226	Sequence 226, Appl
16	1168	99.9	450	4	US-09-986-288-228	Sequence 228, Appl
17	1168	99.9	450	4	US-09-986-288-232	Sequence 232, Appl
18	1168	99.9	450	4	US-09-986-288-234	Sequence 234, Appl
19	1168	99.9	450	4	US-09-986-288-236	Sequence 236, Appl
20	1168	99.9	450	4	US-09-986-288-238	Sequence 238, Appl
21	1168	99.9	450	4	US-09-986-288-240	Sequence 240, Appl
22	1168	99.9	450	4	US-09-986-288-242	Sequence 242, Appl
23	1168	99.9	450	4	US-09-986-288-244	Sequence 244, Appl
24	1168	99.9	450	4	US-09-986-288-246	Sequence 246, Appl
25	1168	99.9	450	4	US-09-986-288-248	Sequence 248, Appl
26	1168	99.9	450	4	US-09-986-288-250	Sequence 250, Appl
27	1168	99.9	450	4	US-09-986-288-252	Sequence 252, Appl

28	1168	99.9	450	4	US-09-986-288-254	Sequence 254, Appl
29	1168	99.9	450	4	US-09-986-288-256	Sequence 256, Appl
30	1168	99.9	451	2	US-08-887-3528-14	Sequence 14, Appl
31	1168	99.9	451	2	US-08-887-3528-16	Sequence 16, Appl
32	1168	99.9	451	2	US-08-887-3528-18	Sequence 18, Appl
33	1168	99.9	451	3	US-08-466-151-65	Sequence 65, Appl
34	1168	99.9	451	3	US-09-109-207C-14	Sequence 14, Appl
35	1168	99.9	451	3	US-09-109-207C-16	Sequence 16, Appl
36	1168	99.9	451	3	US-09-109-207C-18	Sequence 18, Appl
37	1168	99.9	451	3	US-09-282-505-2	Sequence 2, Appl
38	1168	99.9	451	3	US-09-054-255-2	Sequence 2, Appl
39	1168	99.9	451	3	US-09-296-005-14	Sequence 14, Appl
40	1168	99.9	451	3	US-09-296-005-16	Sequence 16, Appl
41	1168	99.9	451	3	US-09-296-005-18	Sequence 18, Appl
42	1168	99.9	451	3	US-09-282-846-2	Sequence 2, Appl
43	1168	99.9	451	4	US-09-680-145-2	Sequence 2, Appl
44	1168	99.9	451	4	US-09-920-171-14	Sequence 14, Appl
45	1168	99.9	451	4	US-09-920-171-16	Sequence 16, Appl
46	1168	99.9	451	4	US-09-920-171-18	Sequence 18, Appl
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ALIGNMENTS

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; Sequence 3, Application US/09483588
; Patent No. 6737056
; GENERAL INFORMATION:
; APPLICANT: Leonard Pirella
; TITLE OF INVENTION: Polypeptide Variance with Altered Effector Function
; FILE REFERENCE: P17261
; CURRENT APPLICATION NUMBER: US/09/483, 588
; EARLIER APPLICATION NUMBER: US 60/116, 023
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 3
; LENGTH: 218
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-483-588-3

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; Sequence 22, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Legier, Olivier
; APPLICANT: Saldanha, Jose W.
; TITLE OF INVENTION: FcR γ -specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301, 593A
; EARLIER FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086, 049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-22

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QY 61 KPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIKRTISKAKGQPREPOVY 120
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QY 121 TLPSRREMTKNQVSLTCLVGFYPSPDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 180
DB 233 TLPSRREMTKNQVSLTCLVGFYPSPDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 292
QY 181 LTVDSRWQCGNVFSCSYMEALHNHTYQKSLSLSPGK 218
DB 293 LTVDSRWQCGNVFSCSYMEALHNHTYQKSLSLSPGK 330

RESULT 3
US-08-775-066-2
; Sequence 2, Application US/08775066

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:17:31 ; Search time 125 Seconds
(without alignments)
674.510 Million cell updates/sec

Title: US-10-757-863-3

Perfect score: 1169
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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XX asthma; LfA-1-mediated disorder; tumour; cancer.
OS Homo sapiens.
XX
PN WO200042072-A2.

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PD 14-JAN-2000; 2000WO-US000973.
XX 15-JAN-1999; 99US-0116023P.
PR (GETH) GENENTECH INC.
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PI WPI; 2000-476035/41.
XX
DR New Fc region-containing polypeptides that have altered effector function
PT due to one or more amino acid modifications in the Fc region, useful in
PT the treatment of cancer and allergic conditions such as asthma.
XX Disclosure; Fig 22A; 132pp; English.
XX
CC AAB07474-78 represent native IgG Fc regions. The proteins are used to
CC produce Fc region-containing polypeptides that have altered effector
CC function as a consequence of one or more amino acid modifications in the
CC Fc region. The variant polypeptides are useful for treating cancer,
CC allergic conditions such as asthma (with an anti-IgE antibody), and LfA-1
CC -mediated disorders. Where the polypeptide binds the HER2 receptor, the
CC disorder preferably is HER2-expressing cancer, e.g. a benign or malignant
CC tumour characterized by overexpression of the HER2 receptor. Such cancers
CC include breast cancer, squamous cell cancer, small-cell lung cancer, non-
CC small cell lung cancer, gastrointestinal cancer, pancreatic cancer,
CC glioblastoma, cervical cancer, ovarian cancer, bladder cancer, hepatoma,
CC colon cancer, colorectal cancer, endometrial carcinoma, salivary gland
CC carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer,
CC thyroid cancer, hepatic carcinoma and various types of head and neck
CC cancer.
XX
SQ Sequence 218 AA;

```

```

Query Match 99.9%; Score 1168; DB 3; Length 218;
Best Local Similarity 99.5%; Pred. No. 3,1e-87;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 PABELLGGPSVFLPFPKPKDTLMSRTPEDTCVVVDVSHEDPEVKENYVDGVEYNAKT 60
DB 1 PABELLGGPSVFLPFPKPKDTLMSRTPEDTCVVVDVSHEDPEVKENYVDGVEYNAKT 60
QY 61 KPREQYXKTRVSVLTVLHQDWLNGKEYCKCKSNKLLPAPIETTSKAGQPREPQVY 120
DB 61 KPREQYXKTRVSVLTVLHQDWLNGKEYCKCKSNKLLPAPIETTSKAGQPREPQVY 120
QY 121 TLPPREEMTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTPPVLDSDGSFFLYSK 180
DB 121 TLPPREEMTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTPPVLDSDGSFFLYSK 180
QY 181 LTVDSKRWQOGNVFSCSVMEALNNHYTKSLISLSPGK 218
DB 181 LTVDSKRWQOGNVFSCSVMEALNNHYTKSLISLSPGK 218

```

```

RESULT 2
AAB76421
ID AAB76421 standard; protein; 218 AA.
XX
AC AAB76421;
XX
DT 10-APR-2001 (first entry)
XX
DE Human IgG1 non-A Fc region amino acid sequence.
XX
KW Human; erBb2; HER2; cancer; nervous system disease; stroke; ischaemia;
XX metabolic disorder; nutritional deficiency; Alzheimer's disease;
XX Parkinson's disease; epilepsy; multiple sclerosis; Huntington's chorea;
XX Down's syndrome; nerve deafness; Meniere's disease; diabetic neuropathy.
XX

```

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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:31:08 ; Search time 25 Seconds

(without alignments)
839.010 Million cell updates/sec

Title: US-10-757-863-4

Perfect score: 1169

Sequence: 1 PAVELIGSGSVFLPPKPKD.....MPEALHNHYTQKSLSLSPGK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1168	99.9	255	4 G3H866	Ig gamma-1 chain C
2	1168	99.9	330	1 GHU	Ig gamma-1 chain C
3	1162	99.4	374	2 S69339	Ig heavy chain V r
4	1122	96.0	234	2 PT0207	Ig gamma chain C r
5	1118	95.6	377	2 A23511	Ig gamma-3 chain C
6	1116	95.5	377	2 A60764	Ig gamma-3 chain C
7	1107	94.7	327	1 G4HU	Ig gamma-4 chain C
8	1106.5	94.7	326	1 G2HU	Ig gamma-2 chain C
9	1093	93.5	289	1 G3HUMI	Ig gamma-3 heavy C
10	892	76.3	323	1 GHRB	Ig gamma chain C r
11	882	75.4	328	2 I47160	Ig gamma 2b chain
12	882	75.4	328	2 I47159	Ig gamma 2a chain
13	876	74.9	277	2 I47162	Ig gamma 4 chain C
14	859	73.5	329	1 G2GP	Ig gamma-2 chain C
15	856	73.2	328	2 I47158	Ig gamma 1 chain C
16	854	73.1	328	2 I47161	Ig gamma 3 chain C
17	835	71.4	470	2 S22080	Ig heavy chain pre
18	831	71.1	308	2 C30554	Ig heavy chain C r
19	831	71.1	472	2 S31459	Ig gamma-1 chain -
20	830	71.0	329	1 G3MSC	Ig gamma-3 chain C
21	819	70.1	328	1 G3MSM	Ig gamma-3 chain C
22	814	69.6	333	1 PS0018	Ig gamma-2b chain
23	811.5	69.4	444	2 PC4436	monoclonal antibod
24	810	68.6	326	2 PS0017	Ig gamma-1 chain C
25	801.5	68.6	329	1 G1MS	Ig gamma-1 chain C
26	800	68.4	329	2 S00847	Ig gamma-2c chain
27	796.5	68.1	333	1 G1MSM	Ig gamma-1 chain C
28	784	67.1	330	1 G2MSA	Ig gamma-2a chain
29	784	67.1	469	2 S37483	Ig gamma-2a chain

30	779	66.6	399	1 G2MSAM	Ig gamma-2a chain
31	778	66.6	322	2 PS0019	Ig gamma-2a chain
32	776	66.4	335	1 G2MSAB	Ig gamma-2a chain
33	769	65.8	446	2 S40295	Ig gamma-2a chain
34	760	65.0	327	2 S06611	Ig gamma-2 chain C
35	756	64.7	474	1 G2MS11	Ig gamma-2b chain
36	751	64.2	405	1 G2MSBM	Ig gamma-2b chain
37	751	62.8	475	2 S01321	Ig gamma-2b chain
38	703	60.1	180	2 I46732	Ig gamma heavy cha
39	576.5	49.3	249	2 S69340	Ig heavy chain VHI
40	574.5	49.1	218	2 A36040	Ig heavy chain V-I
41	567	48.5	152	2 S14236	Ig gamma-1 chain C
42	394	33.7	572	2 B46529	Ig heavy chain (
43	357	30.5	453	2 S37768	Ig mu chain C regi
44	356.5	30.5	549	2 S04845	Ig heavy chain pre
45	355.5	30.4	448	2 S03186	Ig heavy chain C r
46	355	30.4	391	1 MHHUT	Ig mu heavy chain
47	352	30.1	429	1 EHRT	Ig epsilon chain C
48	351	30.0	388	1 EHMS	Ig epsilon chain C
49	348.5	29.8	452	1 MHRU	Ig mu chain C regi
50	348	29.8	426	2 I36948	Ig epsilon-chain -
51	348	29.8	548	2 S38864	Ig epsilon chain C
52	347	29.7	428	1 EHRU	Ig epsilon chain C
53	347	29.7	627	2 S14683	Ig mu chain precu
54	346	29.6	343	2 S25644	Ig mu chain C regi
55	345	29.5	455	1 MHS	Ig mu chain C regi
56	345	29.5	455	1 A24976	Ig mu chain C regi
57	344	29.4	474	2 S15590	Ig heavy chain - h
58	338.5	29.0	473	1 MHRUM	Ig mu chain C regi
59	336.5	28.8	504	2 S00390	Ig gamma chain (c1
60	335	28.7	458	1 MHRB	Ig mu chain C regi
61	335	28.7	476	1 MHRSM	Ig mu chain C regi
62	331	28.3	450	1 MHDG	Ig mu chain C regi
63	329.5	28.2	423	1 EHMS	Ig epsilon chain C
64	327.5	28.0	112	2 B30503	Ig gamma-2a chain
65	327	28.0	454	1 MHRU	Ig mu chain C regi
66	325	27.8	479	1 MHRBM	Ig mu chain C regi
67	322	27.5	457	2 S03961	Ig mu chain C regi
68	321	27.5	592	2 S25705	Ig mu chain - shee
69	312	26.7	453	2 C31933	Ig mu chain C regi
70	296.5	25.4	433	2 S31436	Ig upsilon chain -
71	295	25.2	577	2 I50731	Ig heavy chain - n
72	294	25.1	438	1 HVRK2	Ig mu chain C regi
73	288.5	24.7	342	2 I47175	Ig alpha chain C r
74	286.5	24.5	367	1 MHCH	Ig mu chain C regi
75	281	24.0	438	1 HVRKCS	Ig mu chain C regi
76	277.5	23.7	299	1 AHRB	Ig alpha chain C r
77	277	23.7	343	2 S09272	Ig alpha chain - c
78	272.5	23.3	585	2 A46507	Ig mu chain C regi
79	272	23.3	370	1 HVRKCS	Ig mu chain C regi
80	272	23.3	461	1 HVRKCO	Ig mu chain C regi
81	271.5	23.2	88	2 A30503	Ig gamma-2b chain
82	271.5	23.2	338	2 S09276	Ig alpha chain C r
83	270	23.1	393	1 HVRKCI	Ig mu chain C regi
84	268.5	23.0	684	2 S60266	Ig alpha chain rece
85	267.5	22.9	339	2 S09264	Ig alpha chain C r
86	266.5	22.8	344	2 S12328	Ig heavy chain C r
87	266	22.8	357	2 S09269	Ig alpha chain C r
88	262	22.4	111	2 S43148	Ig upsilon chain -
89	260.5	22.3	357	2 S09265	Ig alpha chain C r
90	258.5	22.1	348	2 S09270	Ig alpha chain C r
91	258.5	22.1	352	2 S09266	Ig alpha chain C r
92	256.5	21.9	348	2 S09273	Ig alpha chain C r
93	255.5	21.9	340	2 I56230	Ig alpha-2 chain -
94	255.5	21.9	340	2 B23360	Ig alpha-2 chain C
95	253.5	21.9	347	2 S09274	Ig alpha chain C r
96	255	21.8	353	1 AIHU	Ig alpha chain C r
97	253.5	21.7	352	2 S05500	Ig alpha-1 chain C
98	253.5	21.7	474	2 I50830	Ig mu chain C regi
99	252.5	21.6	454	2 A46532	Ig mu chain C regi
100	252	21.6	360	2 S09271	Ig alpha chain C r
101	252	21.3	568	2 A34891	Ig heavy chain pre
102	246.5	21.1	340	1 A2HU	Ig alpha-2 chain C

```

103 246 21.0 342 2 A45966 Ig alpha chain C r
104 245.5 21.0 568 2 A45804 Ig mu chain C regi
105 245 21.0 220 2 C22360 Ig alpha-2 chain C
106 245 21.0 357 2 S09267 Ig alpha chain C r
107 241 20.6 573 2 S12838 Ig mu chain precu
108 238.5 20.4 344 1 AHMS Ig alpha chain C r
109 237 20.3 580 2 A46538 Ig heavy chain, se
110 233 19.9 358 2 S09268 Ig alpha chain C r
111 230.5 19.7 335 2 S09275 Ig alpha chain C r
112 209 17.9 115 2 I68731 Ige chain C4 regio
113 206 17.6 448 2 A46533 Ig heavy chain C r
114 203 17.4 402 2 S20002 Ig heavy chain, se
115 202 17.3 115 2 I68727 Ige chain C4 regio
116 201 17.2 228 2 S03050 Ig gamma chain (cl
117 191.5 16.4 140 2 A34509 Ig light chain C r
118 184.5 15.8 233 2 I51383 Ig lambda chain - s
119 184.5 15.8 240 2 A41797 Ig light chain - s
120 183.5 15.7 106 2 S22760 Ig lambda-2 chain
121 183.5 15.7 214 2 PC4156 Ig lambda chain V
122 183.5 15.7 1005 2 TI8537 Ig heavy chain - c
123 182 15.6 212 2 S70431 Ig lambda chain - c
124 181 15.5 102 2 B34509 Ig light chain C r
125 180 15.4 231 2 S25751 Ig lambda chain - c
126 179 15.3 216 2 S03401 Ig lambda chain (K
127 179 15.3 509 2 JCS288 SHP substrate-1 pr
128 179 15.3 513 2 JCS289 SHP substrate-1 pr
129 178 15.2 105 2 B27390 Ig lambda-2 chain
130 178 15.2 227 2 PH1215 Ig epsilon chain C
131 178 15.2 243 2 PH1216 Ig epsilon chain C
132 177.5 15.2 105 1 LIMS Ig lambda-1 chain
133 177 15.1 118 2 A46516 Ig lambda chain J-
134 175 15.0 118 2 A39949 Ig lambda chain C-
135 173 14.8 232 2 S25756 Ig lambda chain J-
136 173 14.8 235 2 S25750 Ig lambda chain - c
137 172 14.7 115 2 E53116 Ig epsilon chain C
138 172 14.7 118 2 C46516 Ig lambda chain C
139 171 14.6 118 2 S12440 Ig lambda chain (M
140 171 14.6 235 2 S25754 Ig lambda chain - c
141 171 14.6 235 2 S25758 Ig lambda chain - c
142 170.5 14.6 118 2 B30505 Ig lambda-6 chain
143 170.5 14.6 232 2 S13993 Ig lambda chain pr
144 170 14.5 118 2 S14443 Ig lambda chain (K
145 169.5 14.5 231 2 PC4155 Ig gamma-2b chain
146 169 14.5 105 2 S22762 Ig lambda-2 chain
147 169 14.5 231 2 S25738 Ig lambda chain - c
148 168.5 14.4 234 2 S25757 Ig lambda chain - c
149 168 14.4 235 2 S05270 Ig lambda chain pr
150 167 14.3 105 2 S22759 Ig lambda-2 chain

```

ALIGNMENTS

```

RESULT 1
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FILL>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-32/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region
Query Match 99.9%; Score 1168; DB 4; Length 255;

```

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Beet Local Similarity 99.5%; Pred. No. 2,36-85;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PAPRLGGPSVFLPPPKKOTLMSRPETCVVVDVSHDEPKFMVYDGVVNAKT 60
38 PAPRLGGPSVFLPPPKKOTLMSRPETCVVVDVSHDEPKFMVYDGVVNAKT 97
DB KPREQYXKTYRVSVTLVTHQDWLNGKEYCKVSNKALPAPIRTISKAKGPREPOVY 120
98 KPREQYXKTYRVSVTLVTHQDWLNGKEYCKVSNKALPAPIRTISKAKGPREPOVY 157
QY 121 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK 180
158 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSK 217
DB 181 LTVDKSRWQGNVSCVMHEALHNHYTQKSLSLSPCK 218
218 LTVDKSRWQGNVSCVMHEALHNHYTQKSLSLSPCK 255

```

RESULT 2

```

GHMU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90564; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: UNIPROT:P01857; EMBL:Z17370
A:Note: this sequence has the Gln(17) alleotypic marker, 97-Lys, and the Gln(1) markers,
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Bu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96, R', 98-135 <CUN>
A:Note: this sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Bu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hillebrand, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nle),
Igen Primärstruktur

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 12:26:52 ; Search time 112.5 Seconds
(without alignments)
992.296 Million cell updates/sec

Title: US-10-757-863-4

Perfect score: 1169
Sequence: 1 PAPELLGGPSVFLPPKPKD.....MKEALHNYTKSLSPGK 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.9	330	1 GCI_HUMAN	P01857 homo sapien
2	1168	99.9	465	2 Q6GMX6	Q6GMX6 homo sapien
3	1168	99.9	466	2 Q6IN78	Q6IN78 homo sapien
4	1168	99.9	469	2 Q7Z7P5	Q7Z7P5 homo sapien
5	1168	99.9	470	2 Q6B2M4	Q6B2M4 homo sapien
6	1168	99.9	470	2 Q7Z5W1	Q7Z5W1 homo sapien
7	1168	99.9	472	2 Q6N089	Q6N089 homo sapien
8	1168	99.9	475	2 Q6GMW7	Q6GMW7 homo sapien
9	1168	99.9	476	2 Q6GKX1	Q6GKX1 homo sapien
10	1168	99.9	679	2 Q6P055	Q6P055 homo sapien
11	1164	99.6	473	2 Q6P055	Q6P055 homo sapien
12	1164	99.6	475	2 Q6M2Q6	Q6M2Q6 homo sapien
13	1164	99.6	480	2 Q6N094	Q6N094 homo sapien
14	1164	99.6	481	2 Q6N097	Q6N097 homo sapien
15	1164	99.6	482	2 Q7Z351	Q7Z351 homo sapien
16	1163	99.5	487	2 Q6S2L2	Q6S2L2 mus sp. fy/
17	1162	99.4	348	2 Q6PYX1	Q6PYX1 homo sapien
18	1162	99.4	473	2 Q6M2V7	Q6M2V7 homo sapien
19	1162	99.4	478	2 Q6P181	Q6P181 homo sapien
20	1162	99.4	480	2 Q6P1F1	Q6P1F1 homo sapien
21	1161	99.3	466	2 Q6N096	Q6N096 homo sapien
22	1157	99.0	475	2 Q6N095	Q6N095 homo sapien
23	1157	99.0	544	2 Q6P095	Q6P095 homo sapien
24	1118	95.6	354	2 Q6B7T2	Q6B7T2 homo sapien
25	1118	95.6	518	2 Q6N030	Q6N030 homo sapien
26	1114	95.3	521	2 Q6N4Y9	Q6N4Y9 homo sapien
27	1107	94.7	327	1 GCA_HUMAN	P01861 homo sapien
28	1107	94.7	473	2 Q6T6C3	Q6T6C3 homo sapien
29	1106.5	94.7	326	1 GCI_HUMAN	P01859 homo sapien
30	1106.5	94.7	417	2 Q6N093	Q6N093 homo sapien
31	1103.5	94.4	464	2 Q6M2U6	Q6M2U6 homo sapien

32	1103	94.4	509	2 Q6NP17	Q6NP17 homo sapien
33	1101.5	94.2	465	2 Q6P6C4	Q6P6C4 homo sapien
34	1098	93.9	290	1 GCI_HUMAN	P01860 homo sapien
35	1098	93.9	476	2 Q6MZX7	Q6MZX7 homo sapien
36	1092.5	93.5	493	2 Q6B2M4	Q6B2M4 homo sapien
37	892	76.3	323	1 GCI_RABIT	P01870 oryctolagus
38	881	75.4	337	2 Q6SM34	Q6SM34 equus caball
39	859	72.5	329	1 GCI_CAVPO	P01862 cavia porce
40	830	71.0	329	1 GCI_MOUSE	P22436 mus musculus
41	830	71.0	470	2 Q7TMK1	Q7TMK1 mus musculus
42	819	70.1	303	2 Q6KAM2	Q6KAM2 mus musculus
43	819	70.1	398	1 GCI_MOUSE	P01868 mus musculus
44	814	69.6	333	1 GCI_RAT	P20761 rattus norv
45	812.5	69.5	463	2 Q6S2Q1	Q6S2Q1 mus musculus
46	811.5	69.4	458	2 Q6S2Q1	Q6S2Q1 mus musculus
47	810	69.3	326	1 GCI_RAT	P20759 rattus norv
48	801.5	68.6	324	1 GCI_MOUSE	P01868 mus musculus
49	800	68.4	329	1 GCI_MOUSE	P20762 rattus norv
50	796.5	68.1	393	1 GCI_MOUSE	P01869 mus musculus
51	784	67.1	330	1 GCI_MOUSE	P01863 mus musculus
52	784	67.1	464	2 Q6P1F9	Q6P1F9 mus musculus
53	780	66.7	464	2 Q6P1P8	Q6P1P8 mus musculus
54	780	66.7	465	2 Q6P1B2	Q6P1B2 mus musculus
55	780	66.7	471	2 Q6K0Y4	Q6K0Y4 mus musculus
56	780	66.7	472	2 Q6P0A7	Q6P0A7 mus musculus
57	779	66.6	399	1 GCI_MOUSE	P01865 mus musculus
58	778	66.6	322	1 GCI_RAT	P20760 rattus norv
59	776	66.4	335	1 GCI_MOUSE	P01864 mus musculus
60	776	66.4	473	2 Q6D814	Q6D814 mus musculus
61	757	64.8	473	2 Q6I205	Q6I205 mus musculus
62	757	64.8	474	2 Q6R3H6	Q6R3H6 mus musculus
63	756	64.7	336	1 GCI_MOUSE	P01866 mus musculus
64	751	64.2	305	1 GCI_MOUSE	P01867 mus musculus
65	357	30.5	475	2 Q6B7T1	Q6B7T1 mus musculus
66	357	30.5	454	1 GCI_HUMAN	P01871 homo sapien
67	357	30.5	597	2 Q6B2B9	Q6B2B9 homo sapien
68	357	30.5	597	2 Q6GAM5	Q6GAM5 homo sapien
69	357	30.5	597	2 Q6B0B8	Q6B0B8 homo sapien
70	357	30.5	597	2 Q6B0B8	Q6B0B8 homo sapien
71	357	30.5	606	2 Q6GMY2	Q6GMY2 homo sapien
72	355	30.4	391	1 GCI_HUMAN	P04220 homo sapien
73	354.5	30.3	585	2 Q6GPK4	Q6GPK4 xenopus lae
74	352	30.1	429	1 GCI_RAT	P01855 rattus norv
75	351	30.0	421	1 GCI_MOUSE	P06336 mus musculus
76	348.5	29.8	584	2 Q6INK3	Q6INK3 xenopus lae
77	347	29.7	428	1 GCI_HUMAN	P01854 homo sapien
78	347	29.7	595	2 Q6WUX4	Q6WUX4 homo sapien
79	347	29.7	613	2 Q6WUX4	Q6WUX4 homo sapien
80	347	29.7	620	2 Q6EYX0	Q6EYX0 homo sapien
81	347	29.7	625	2 Q6EYX0	Q6EYX0 homo sapien
82	345	29.5	455	1 GCI_MOUSE	P01872 mus musculus
83	337	28.8	614	2 Q7TMT6	Q7TMT6 mus musculus
84	335	28.7	458	1 GCI_RABIT	P01873 mus musculus
85	335	28.7	476	1 GCI_MOUSE	P01873 mus musculus
86	335	28.3	613	2 Q6VXC7	Q6VXC7 mus musculus
87	331	28.3	450	1 GCI_CANFA	P01874 canis fam1
88	325	27.8	454	1 GCI_RABIT	P04221 oryctolagus
89	324	27.7	459	1 GCI_MOUSE	P06337 mesocricetu
90	322	27.5	457	1 GCI_MOUSE	P20768 suncus murt
91	315	26.9	572	2 Q6I0I7	Q6I0I7 xenopus lae
92	312	26.7	587	2 Q7TOR1	Q7TOR1 xenopus lae
93	312	26.7	588	2 Q6IR66	Q6IR66 xenopus lae
94	312	26.7	593	2 Q6INM5	Q6INM5 xenopus lae
95	312	26.7	605	2 Q6GAM3	Q6GAM3 xenopus lae
96	306	26.2	614	2 Q6DDO7	Q6DDO7 xenopus lae
97	294	25.1	438	1 GCI_HETER	P23085 heterodontu
98	286.5	24.5	446	1 GCI_CHICK	P01875 gallus gall
99	281	24.0	438	1 GCI_HETER	P23087 heterodontu
100	277.5	23.7	299	1 GCI_RABIT	P01879 oryctolagus
101	272	23.3	370	1 GCI_HETER	P23084 heterodontu
102	272	23.3	461	1 GCI_HETER	P23088 heterodontu
103	270	23.1	393	1 GCI_HETER	P23086 heterodontu
104	268.5	23.0	684	2 Q6S544	Q6S544 ginglymosco

105	257.5	22.0	478	2	Q7Z379	Q7Z379	homo sapien
106	257.5	22.0	492	2	Q7Z374 <td>Q7Z374 <th>homo sapien</th> </td>	Q7Z374 <th>homo sapien</th>	homo sapien
107	255.5	21.9	340	1	ALC2 HUMAN	P01877 <th>homo sapien</th>	homo sapien
108	255.5	21.9	416	2	Q9NPB6	Q9NPB6 <th>homo sapien</th>	homo sapien
109	255.5	21.9	477	2	Q6CMX7	Q6CMX7 <th>homo sapien</th>	homo sapien
110	255.5	21.9	478	2	Q6MYH3	Q6MYH3 <th>homo sapien</th>	homo sapien
111	255.5	21.9	479	2	Q6MZV6	Q6MZV6 <th>homo sapien</th>	homo sapien
112	255.5	21.9	480	2	Q6P089	Q6P089 <th>homo sapien</th>	homo sapien
113	255.5	21.9	483	2	Q6MZK9	Q6MZK9 <th>homo sapien</th>	homo sapien
114	255.5	21.9	487	2	Q6ZYX0	Q6ZYX0 <th>homo sapien</th>	homo sapien
115	255	21.8	353	1	ALC1 HUMAN	P01876 <th>homo sapien</th>	homo sapien
116	255	21.8	384	2	Q9UP60	Q9UP60 <th>homo sapien</th>	homo sapien
117	255	21.8	493	2	Q8NCL6	Q8NCL6 <th>homo sapien</th>	homo sapien
118	255	21.8	493	2	Q6GMX2	Q6GMX2 <th>homo sapien</th>	homo sapien
119	255	21.8	494	2	Q6KXK8	Q6KXK8 <th>homo sapien</th>	homo sapien
120	255	21.8	496	2	Q6KXK8	Q6KXK8 <th>homo sapien</th>	homo sapien
121	255	21.8	506	2	Q6MZW0	Q6MZW0 <th>homo sapien</th>	homo sapien
122	255	21.8	506	2	Q6N090	Q6N090 <th>homo sapien</th>	homo sapien
123	254.5	21.8	498	2	Q6N041	Q6N041 <th>homo sapien</th>	homo sapien
124	254.5	21.8	500	2	Q6N091	Q6N091 <th>homo sapien</th>	homo sapien
125	253.5	21.7	353	1	ALC1 GORGO	P20758 <th>gorilla gor</th>	gorilla gor
126	252	21.6	494	2	Q6ZM64	Q6ZM64 <th>homo sapien</th>	homo sapien
127	252	21.6	496	2	Q6DK0	Q6DK0 <th>homo sapien</th>	homo sapien
128	252	21.6	499	2	Q8NSK4	Q8NSK4 <th>homo sapien</th>	homo sapien
129	252	21.6	519	2	Q6N092	Q6N092 <th>homo sapien</th>	homo sapien
130	250	21.4	497	2	Q8WY24	Q8WY24 <th>homo sapien</th>	homo sapien
131	250	21.4	500	2	Q9BRV0	Q9BRV0 <th>homo sapien</th>	homo sapien
132	245.5	21.0	481	1	MUCM ICTRU	P23735 <th>ictalurus p</th>	ictalurus p
133	241.5	20.7	481	2	Q91WT1	Q91WT1 <th>mus musculus</th>	mus musculus
134	241.5	20.7	481	2	Q91WT3	Q91WT3 <th>mus musculus</th>	mus musculus
135	241.5	20.7	482	2	Q91X92	Q91X92 <th>mus musculus</th>	mus musculus
136	241.5	20.7	482	2	Q8K172	Q8K172 <th>mus musculus</th>	mus musculus
137	241.5	20.7	484	2	Q8VEA0	Q8VEA0 <th>mus musculus</th>	mus musculus
138	241.5	20.7	485	2	Q6PDB8	Q6PDB8 <th>mus musculus</th>	mus musculus
139	241.5	20.7	487	2	Q80Z17	Q80Z17 <th>mus musculus</th>	mus musculus
140	241.5	20.7	488	2	Q8K0F2	Q8K0F2 <th>mus musculus</th>	mus musculus
141	241.5	20.7	488	2	Q91MR1	Q91MR1 <th>mus musculus</th>	mus musculus
142	241.5	20.7	489	2	Q8VCX4	Q8VCX4 <th>mus musculus</th>	mus musculus
143	239.5	20.5	479	2	Q91WPS	Q91WPS <th>mus musculus</th>	mus musculus
144	238.5	20.4	344	1	ALC1 MOUSE	P01878 <th>mus musculus</th>	mus musculus
145	238.5	20.4	479	2	Q9PM22	Q9PM22 <th>mus musculus</th>	mus musculus
146	238.5	20.4	479	2	Q7TMK4	Q7TMK4 <th>mus musculus</th>	mus musculus
147	238.5	20.4	480	2	Q91XEL	Q91XEL <th>mus musculus</th>	mus musculus
148	238.5	20.4	480	2	Q8K0Z4	Q8K0Z4 <th>mus musculus</th>	mus musculus
149	238.5	20.4	481	2	Q8VCV5	Q8VCV5 <th>mus musculus</th>	mus musculus
150	238.5	20.4	484	2	Q991A6	Q991A6 <th>mus musculus</th>	mus musculus

ALIGNMENTS

RESULT 1

ID	GCL_HUMAN	STANDARD	PRT	330 AA
AC	P01857			
DT	21-JUL-1966 (Rel. 01, Created)			
DT	21-JUL-1966 (Rel. 01, Last sequence update)			
DT	25-OCT-2004 (Rel. 05, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	Name=IGHG1			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.D., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079 (1982).			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			

RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
 RA Maxdal M.J., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
 RL Biochemistry 9:3161-3170 (1970).
 [3]
 RP SEQUENCE OF 136-329 (EU).
 RX MEDLINE=71064025; PubMed=5530842;
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
 RA Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
 RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
 RL Biochemistry 9:3171-3181 (1970).
 [4]
 RP SEQUENCE (MYELOMA PROTEIN NIE).
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponsingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
 RT peptides of the H-chain, alignment of the tryptic peptides and
 RT discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
 [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
 RX MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).
 [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196 (1970).
 [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie). I: purification and
 RT characterization of the protein, the L- and H-chains, the cyanogen
 RT bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).
 [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from *Staphylococcus*
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370 (1981).
 [9]
 RP MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC GIM(3) marker and the GIM (non-1) markers.
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
 CC 116, 198, 269 and 272.
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL/J00028; AAC82527.1; ALT_INIT.

DR PIR; A93433; GHMU.
 DR PDB; 1A7; X-ray; H=1-103.
 DR PDB; 1D5B; X-ray; B/H=1-101.
 DR PDB; 1D5I; X-ray; H=1-101.
 DR PDB; 1D6V; X-ray; H=1-101.
 DR PDB; 1DN2; X-ray; A/B=120-326.
 DR PDB; 1E4K; X-ray; A/B=106-329.
 DR PDB; 1FCL; X-ray; A/B=106-329.
 DR PDB; 1FCC; X-ray; D=106-329.
 DR PDB; 1FCC; X-ray; A=121-326.
 DR PDB; 1H2H; X-ray; H/K=1-330.
 DR PDB; 1I7Z; X-ray; B/D=1-103.
 DR PDB; 1I1S; X-ray; A/B=107-330.
 DR PDB; 1I1X; X-ray; A/B=107-330.
 DR PDB; 1L6X; X-ray; A=120-326.
 DR PDB; 1LOK; X-ray; A/B=119-330.
 DR PDB; 2RCS; X-ray; H=1-103.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; .
 DR GO; GO:0005624; C:membrane fraction; NMS.
 DR GO; GO:0003823; P:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-1ike.
 DR InterPro; IPR00306; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR PROSITE; PSS0835; IG_LIKE; 3.
 DR PROSITE; PSS0290; IG_MHC; 2.
 KW 3D-structure; Direct protein sequencing; Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.
 KM NON_TER 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 Hinge.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISUFID 27 83 Interchain (with light chain).
 FT DISUFID 103 103 Interchain (with heavy chain).
 FT DISUFID 109 109 Interchain (with heavy chain).
 FT DISUFID 112 112 Interchain (with heavy chain).
 FT DISUFID 144 204
 FT DISUFID 250 308
 FT CARBOHYD 180 180
 FT VARIANT 97 97
 FT VARIANT 239 239 N-linked (GlcNAc...).
 FT VARIANT 241 241 K -> R (in GIM(3) marker).
 FT VARIANT 241 241 /FtId=VAR_003886.
 FT VARIANT 241 241 D -> E (in GIM(non-1) marker).
 FT VARIANT 241 241 /FtId=VAR_003887.
 FT VARIANT 241 241 L -> M (in GIM(non-1) marker).
 FT VARIANT 241 241 /FtId=VAR_003888.
 FT STRAND 23 24
 FT STRAND 26 33
 FT STRAND 38 38
 FT STRAND 41 41
 FT TURN 42 45
 FT TURN 48 49
 FT STRAND 50 52
 FT STRAND 57 58
 FT TURN 59 61
 FT STRAND 62 71
 FT STRAND 73 75
 FT HELIX 76 78
 FT TURN 82 87
 FT STRAND 88 91
 FT TURN 92 97
 FT TURN 102 103
 FT STRAND 122 126
 FT STRAND 130 134
 FT HELIX 136 137
 FT TURN 141 149
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 167
 FT STRAND 171 172
 FT STRAND 176 177
 FT TURN 179 180

FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 207
 FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 242
 FT STRAND 245 256
 FT STRAND 261 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 311
 FT TURN 313 314
 FT HELIX 316 318
 FT STRAND 319 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EB106C2FA33D CRC64;
 Query Match 99.9%; Score 1168; DB 1; Length 330;
 Best Local Similarity 99.5%; Pred. No. 5,5e-88;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PAPELLGGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 60
 DB 113 PAPELLGGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 172
 QY 61 KPREEQYNKYRVSVLTITVLDHDLNGKEYCKVSNKALPAPIEKTISRKAGQPREPQVY 120
 DB 173 KPREEQYNKYRVSVLTITVLDHDLNGKEYCKVSNKALPAPIEKTISRKAGQPREPQVY 232
 QY 121 TLPPSRDELTKQVSLTCLVKGFPESDI AVEWESNQPENNYKTPPVLDSDGSPFLYSK 180
 DB 233 TLPPSRDELTKQVSLTCLVKGFPESDI AVEWESNQPENNYKTPPVLDSDGSPFLYSK 292
 QY 181 LITDKSRNOQGNVFCSCVNHKALHNHYTQKSLSLSPGK 218
 DB 293 LITDKSRNOQGNVFCSCVNHKALHNHYTQKSLSLSPGK 330
 RESULT 2
 Q6GMX6 PRELIMINARY; PRT; 465 AA.
 AC Q6GMX6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Heich F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Spletton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.P., Mulhally S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073766; AAH73766.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00654; Cl-set; 3.
 DR Pfam; PF00447; Ig; 4.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; Igcl; 3.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 KW SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
 SQ

Query Match 99.9%; Score 1168; DB 2; Length 465;
 Best Local Similarity 99.5%; Pred. No. 8.3e-88;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PAPERLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKT 60
 DB 248 PAPERLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKT 307
 OY 61 KPREEQYNXYTVRVSVLTVLHODMNLNGEKYCKCKVSNKALPAPIETKISKAKGQPREPQVY 120
 DB 308 KPREEQYNXYTVRVSVLTVLHODMNLNGEKYCKCKVSNKALPAPIETKISKAKGQPREPQVY 367
 OY 121 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSK 180
 DB 368 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSK 427
 OY 181 LTVDKSRWQOGNVFSCVMEHALLHNHYTQKSLSLSPGK 218
 DB 428 LTVDKSRWQOGNVFSCVMEHALLHNHYTQKSLSLSPGK 465

RESULT 3

ID 061N78 PRELIMINARY; PRT; 466 AA.
 AC 061N78;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Searse M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Caraminci P., Pirange C.,
 RA Raha S.S., Loguélino N.A., Peters G.J., Abrahams R.D., Mullaly S.J.,
 RA Bosak S.A., McGraw P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC072419; AAH72419.1; -.
 DR HSSP; P01861; IADO.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00654; Cl-set; 3.
 DR Pfam; PF00447; Ig; 4.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; Igcl; 3.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR SEQUENCE 466 AA; 50853 MW; 53EB0BCDEB81076E CRC64;
 SQ

Query Match 99.9%; Score 1168; DB 2; Length 466;
 Best Local Similarity 99.5%; Pred. No. 8.3e-88;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PAPERLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKT 60
 DB 249 PAPERLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKT 308
 OY 61 KPREEQYNXYTVRVSVLTVLHODMNLNGEKYCKCKVSNKALPAPIETKISKAKGQPREPQVY 120
 DB 309 KPREEQYNXYTVRVSVLTVLHODMNLNGEKYCKCKVSNKALPAPIETKISKAKGQPREPQVY 368
 OY 121 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSK 180
 DB 369 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSK 428
 OY 181 LTVDKSRWQOGNVFSCVMEHALLHNHYTQKSLSLSPGK 218
 DB 429 LTVDKSRWQOGNVFSCVMEHALLHNHYTQKSLSLSPGK 466

RESULT 4

ID 0727P5 PRELIMINARY; PRT; 469 AA.
 AC 0727P5;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE IGHG1 protein.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,